

This listing of claims will replace all prior versions and listings of claims in the application:

**Listing of Claims:**

- 1-31. (canceled)
32. (currently amended) A method of detecting a variant CGI-69 polynucleotide in a sample,  
comprising detecting a polynucleotide encoding a polypeptide comprising an amino acid  
sequence having at least 98% sequence identity to SEQ ID NO:3a~~polynucleotide~~  
~~comprising a nucleic acid sequence of SEQ ID NOs:1 or 2.~~
- 33-34. (canceled)
35. (previously presented) The method of claim 32, wherein the ~~nucleic acid sequence~~  
polynucleotide is SEQ ID NO:1.
- 36-37. (canceled)
38. (currently amended) The method of claim 32, wherein the detecting comprises  
amplifying the polynucleotide sequence with a primer ~~comprising a nucleic acid sequence of~~  
~~SEQ ID NO:1 or 2 by polymerase chain reaction.~~
39. (currently amended) The method of claim 32, wherein the detecting comprises  
hybridizing a probe to the polynucleotide ~~comprising a nucleic acid sequence of SEQ ID NO:1~~  
~~or 2.~~
40. (canceled)
41. (previously presented) The method of claim 40, wherein the sample is from a mammal.
42. (previously presented) The method of claim 41, wherein the sample is from a human.

43. (currently amended) The method of claim 40, wherein the sample ~~comprises at least one member selected from the group consisting of~~ is blood, serum, cells, and tissue, or combinations thereof.

44. (currently amended) A method of detecting a variant CGI-69 polynucleotide in a sample, comprising:

(a) contacting the sample with a nucleic acid probe that hybridizes to a polynucleotide encoding a polypeptide comprising an amino acid sequence having at least 98% sequence identity to SEQ ID NO:3 under stringent conditions~~hybridizing under stringent conditions a probe comprising at least a portion of a polynucleotide comprising a nucleic acid sequence of SEQ ID NO:1 or 2 to a nucleic acid sample; and~~

(b) identifying the CGI-69 polynucleotide in the sample by detecting a hybridization signal.

45. (canceled)

46. (currently amended) The method of claim 45, wherein the ~~encoded~~ polypeptide comprises the amino acid sequence of SEQ ID NO:3.

47. (canceled)

48. (currently amended) The method of claim ~~44~~ 45, wherein the detecting comprises amplifying the polynucleotide sequence with a primer ~~encoding an amino acid sequence of SEQ ID NO:3 or 4 by polymerase chain reaction.~~

49. (currently amended) The method of claim ~~44~~ 45, wherein the detecting comprises hybridizing a probe to the polynucleotide ~~encoding a polypeptide comprising an amino acid sequence of SEQ ID NO:3 or 4.~~

50. (canceled)
51. (currently amended) The method of claim ~~50~~44, wherein the sample is from a mammal.
52. (previously presented) The method of claim 51, wherein the sample is from a human.
53. (currently amended) The method of claim ~~50~~44, wherein the sample ~~comprises at least one member selected from the group consisting of~~ is blood, serum, cells, and tissue, or combinations thereof.
54. (new) The method of claim 32, wherein the polynucleotide comprises SEQ ID NO:1.
55. (new) The method of claim 39, wherein the probe hybridizes to the polynucleotide or its complement under stringent conditions.
56. (new) The method of claim 55, wherein the probe comprises SEQ ID NO:11, SEQ ID NO:12, or SEQ ID NO:14.
57. (new) The method of claim 55, wherein the polynucleotide comprises a nucleic acid sequence corresponding to nucleotides 265 to 288 of SEQ ID NO:1.
58. (new) The method of claim 38, wherein the polynucleotide sequence amplified comprises a nucleic acid sequence of SEQ ID NO:1.
59. (new) The method of claim 39, wherein the probe hybridizes to a polynucleotide comprising a nucleic acid sequence of SEQ ID NO:1.
60. (new) The method of claim 55, wherein the polynucleotide comprises a nucleic acid sequence that encodes an amino acid sequence corresponding to amino acid residues 65 to 72 of SEQ ID NO:3.

61. (new) The method of claim 60, wherein the probe hybridizes at least to the nucleic acid sequence that encodes an amino acid sequence corresponding to amino acid residues 65 to 72 of SEQ ID NO:3.
62. (new) The method of claim 32, wherein the oligonucleotide is a primer that hybridizes to the polynucleotide or its complement under stringent conditions.
63. (new) The method of claim 32, wherein the polypeptide is localized in the mitochondrial membrane.
64. (new) The method of claim 44, wherein the polynucleotide comprises SEQ ID NO:1.
65. (new) The method of claim 44, wherein the polynucleotide comprises a nucleic acid sequence corresponding to nucleotides 265 to 288 of SEQ ID NO:1.
66. (new) The method of claim 64, wherein wherein the probe hybridizes to a polynucleotide encoding an amino acids sequence comprising SEQ ID NO:3.
67. (new) The method of claim 44, wherein the polynucleotide comprises a nucleic acid sequence that encodes an amino acid sequence corresponding to amino acid residues 65 to 72 of SEQ ID NO:3.
68. (new) The method of claim 66, wherein the nucleic acid probe hybridizes at least to the nucleic acid sequence that encodes an amino acid sequence corresponding to amino acid residues 65 to 72 of SEQ ID NO:3.
69. (new) The method of claim 44, wherein the nucleic acid probe comprises SEQ ID NO:11, SEQ ID NO:12, or SEQ ID NO:13.

70. (new) The method of claim 44, wherein the polynucleotide sequence amplified encodes a polypeptide comprising an amino acid sequence of SEQ ID NO:3.

69. (new) The method of claim 44, wherein the polypeptide is localized in the mitochondrial membrane.

70. (new) The method of claim 43, wherein the tissue is adipose tissue.

71. (new) The method of claim 53, wherein the tissue is adipose tissue.